



~~SEQUENCE LISTING~~

(1) GENERAL INFORMATION:

- (i) APPLICANT: QUENTIN-MILLET, Marie-Jose et al.
- (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN RECEPTOR OF NEISSERIA MENINGITIDIS
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LARSON AND TAYLOR
 - (B) STREET: 727 SOUTH 23RD STREET
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: USA
 - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

B

- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/591,447
 - (B) FILING DATE: 29-JAN-1996
 - (C) CLASSIFICATION:

- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: SARRO, THOMAS P
 - (B) REGISTRATION NUMBER: 19,196
 - (C) REFERENCE/DOCKET NUMBER: XI/P02956

- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-920-7200
 - (B) TELEFAX: 703-892-8428

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Neisseria meningitidis
 - (B) STRAIN: IM2169

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 60..119

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 120..2192

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 60..2192

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 120..1154

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1155..1748

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1749..2192

(ix) FEATURE:
(A) NAME/KEY: misc_binding
(B) LOCATION: 237..1169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTTGTTAAA AATAAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT 59
ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5
TTG TTG AGT GCC TGT CTG GGC GGC GGC AGT TTC GAT CTT GAT TCT 155
Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10
GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25
TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG 251
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40
ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG 299
Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu
45 50 55 60

GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys 65 70 75	347
CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu 80 85 90	395
ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser 95 100 105	443
AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn 110 115 120	491
CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe 125 130 135 140	539
TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys 145 150 155	587
TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg 160 165 170	635
<i>B</i> <i>cont.</i> CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe 175 180 185	683
GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro 190 195 200	731
TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser 205 210 215 220	779
GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu 225 230 235	827
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys 240 245 250	875
TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr 255 260 265	923

AAT AAT GAC AAA CAT ACC ACC CAA TAC TAC AGC CTT GAT GCA CAA ATA Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile 270 275 280	971
ACA GGC AAC CGC TTC AAC GGC ACG GCA ACG GCA ACT GAC AAA AAA GAG Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu 285 290 295 300	1019
AAT GAA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser 305 310 315	1067
GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT TTC CGC TTT TTG Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu 320 325 330	1115
AGC GAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC AAA GAC Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp 335 340 345	1163
AAA CTG GAA AAT GGC GCG GCG GCT TCA GGC AGC ACA GGT GCG GCA GCA Lys Leu Glu Asn Gly Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala 350 355 360	1211
TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr 365 370 375 380	1259
GTT TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn 385 390 395	1307
CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met 400 405 410	1355
ATT CCG CTC CTG CCC AAG GAT TCC GAA AGC GGG AAC ACT CAG GCA GAT Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp 415 420 425	1403
AAA GGT AAA AAC GGC GGA ACA GAA TTT ACC CGC AAA TTT GAA CAC ACG Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr 430 435 440	1451
CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly 445 450 455 460	1499
GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys 465 470 475	1547

ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC	1595
Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr	
480 485 490	
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA	1643
Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly	
495 500 505	
AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG	1691
Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met	
510 515 520	
TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA	1739
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln	
525 530 535 540	
AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA	1787
Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr	
545 550 555	
AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA	1835
Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu	
560 565 570	
6 TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT	1883
Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala	
575 580 585	
GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC	1931
Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly	
590 595 600	
AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC	1979
Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu	
605 610 615 620	
GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC	2027
Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala	
625 630 635	
AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA	2075
Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
640 645 650	
TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA	2123
Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr	
655 660 665	
TCC AGC GAT GGA AAT TCA GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG	2171
Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala	
670 675 680	

AAA CGC CAA CAG CCT GTG CAA TAAGCACGGT TGCCGAACAA TCAAGAATAA
Lys Arg Gln Gln Pro Val Gln
685 690

2222

GGCTTCAG

2230

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu
45 50 55 60

Val Lys Leu Asn Glu Ser Asp Trp Gln Ala Thr Gly Leu Pro Thr Lys
65 70 75

Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu
80 85 90

Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser
95 100 105

Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn
110 115 120

Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe
125 130 135 140

Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys
145 150 155

Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg
160 165 170

Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe
175 180 185

Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro
190 195 200

Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser
205 210 215 220

Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu
225 230 235

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys
240 245 250

Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr
255 260 265

Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile
270 275 280

Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu
285 290 295 300

Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
305 310 315

Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu
320 325 330

β
Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp
335 340 345

Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala
350 355 360

Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr
365 370 375 380

Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn
385 390 395

Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
400 405 410

Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp
415 420 425

Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr
430 435 440

Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
445 450 455 460

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
 465 470 475

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
 480 485 490

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
 495 500 505

Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
 510 515 520

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln
 525 530 535 540

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
 545 550 555

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
 560 565 570

Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala
 575 580 585

Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly
 590 595 600

Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
 605 610 615 620

Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
 625 630 635

Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
 640 645 650

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr
 655 660 665

Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
 670 675 680

Lys Arg Gln Gln Pro Val Gln
 685 690

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1808 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..1797

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1797

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 61..1035

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1036..1386

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1387..1797

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
- (B) LOCATION: 46..1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

TTG TTG AGT GCT TGT CTG GGT GGC GGC AGT TTC GAT TTG GAC AGC 96
Leu Leu Ser Ala Cys Leu Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

GTG GAA ACC GTG CAA GAT ATG CAC TCC AAA CCT AAG TAT GAG GAT GAA 144
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
15 20 25

AAA AGC CAG CCT GAA AGC CAA CAG GAT GTA TCG GAA AAC AGC GGC GCG 192
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
30 35 40

GCT TAT GGC TTT GCA GTA AAA CTA CCT CGC CGG AAT GCA CAT TTT AAT 240
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
45 50 55 60

CCT AAA TAT AAG GAA AAG CAC AAA CCA TTG GGT TCA ATG GAT TGG AAA Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys 65 70 75	288
AAA CTG CAA AGA GGA GAA CCA AAT AGT TTT AGT GAG AGG GAT GAA TTG Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu 80 85 90	336
GAA AAA AAA CGG GGT AGT TCT GAA CTT ATT GAA TCA AAA TGG GAA GAT Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp 95 100 105	384
GGG CAA AGT CGT GTA GTT GGT TAT ACA AAT TTC ACT TAT GTC CGT TCG Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser 110 115 120	432
GGA TAT GTT TAC CTT AAT AAA AAT AAT ATT GAT ATT AAG AAT AAT ATA Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile 125 130 135 140	480
GTT CTT TTT GGA CCT GAC GGA TAT CTT TAC TAT AAA GGG AAA GAA CCT Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro 145 150 155	528
TCC AAG GAG CTG CCA TCG GAA AAG ATA ACT TAT AAA GGT ACT TGG GAT Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp 160 165 170	576
TAT GTT ACT GAT GCT ATG GAA AAA CAA AGG TTT GAA GGA TTG GGT AGT Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser 175 180 185	624
GCA GCA GGA GGA GAT AAA TCG GGG GCG TTG TCT GCA TTA GAA GAA GGG Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly 190 195 200	672
GTA TTG CGT AAT CAG GCA GAG GCA TCA TCC GGT CAT ACC GAT TTT GGT Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly 205 210 215 220	720
ATG ACT AGT GAG TTT GAG GTT GAT TTT TCT GAT AAA ACA ATA AAG GGC Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly 225 230 235	768
ACA CTT TAT CGT AAC AAC CGT ATT ACT CAA AAT AAT AGT GAA AAC AAA Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys 240 245 250	816
CAA ATA AAA ACT ACG CGT TAC ACC ATT CAA GCA ACT CTT CAC GGC AAC Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn 255 260 265	864

CGT TTC AAA GGT AAG GCG TTG GCG GCA GAT AAA GGT GCA ACA AAT GGA	912
Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly	
270 275 280	
AGT CAT CCC TTT ATT TCC GAC TCC GAC AGT TTG GAA GGC GGA TTT TAC	960
Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr	
285 290 295 300	
GGG CCG AAA GGC GAG GAA CTT GCC GGT AAA TTC TTG AGC AAC GAC AAC	1008
Gly Pro Lys Gly Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn	
305 310 315	
AAA GTT GCA GCG GTG TTT GGT GCG AAG CAG AAA GAT AAG AAG GAT GGG	1056
Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly	
320 325 330	
GAA AAC GCG GCA GGG CCT GCA ACG GAA ACC GTG ATA GAT GCA TAC CGT	1104
Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg	
335 340 345	
ATT ACC GGC GAG GAG TTT AAG AAA GAG CAA ATA GAC AGT TTT GGA GAT	1152
Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp	
350 355 360	
GTG AAA AAG CTG CTG GTT GAC GGA GTG GAG CTT TCA CTG CTG CCG TCT	1200
Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser	
365 370 375 380	
GAG GGC AAT AAG GCG GCA TTT CAG CAC GAG ATT GAG CAA AAC GGC GTG	1248
Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val	
385 390 395	
<i>b y.</i>	
AAG GCA ACG GTG TGT TGT TCC AAC TTG GAT TAC ATG AGT TTT GGG AAG	1296
Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys	
400 405 410	
CTG TCA AAA GAA AAT AAA GAC GAT ATG TTC CTG CAA GGT GTC CGC ACT	1344
Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr	
415 420 425	
CCA GTA TCC GAT GTG GCG GCA AGG ACG GAG GCA AAC GCC AAA TAT CGC	1392
Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg	
430 435 440	
GGT ACT TGG TAC GGA TAT ATT GCC AAC GGC ACA AGC TGG AGC GGC GAA	1440
Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu	
445 450 455 460	
GCC TCC AAT CAG GAA GGT GGT AAT AGG GCA GAG TTT GAC GTG GAT TTT	1488
Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe	
465 470 475	

TCC ACT AAA AAA ATC AGT GGC ACA CTG ACG GCA AAA GAC CGT ACG TCT Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser 480 485 490	1536
CCT GCG TTT ACT ATT ACT GCC ATG ATT AAG GAC AAC GGT TTT TCA GGT Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly 495 500 505	1584
GTG GCG AAA ACC GGT GAA AAC GGC TTT GCG CTG GAT CCG CAA AAT ACC Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr 510 515 520	1632
GGA AAT TCC CAC TAT ACG CAT ATT GAA GCC ACT GTA TCC GGC GGT TTC Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe 525 530 535 540	1680
TAC GGC AAA AAC GCC ATC GAG ATG GGC GGA TCG TTC TCA TTT CCG GGA Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly 545 550 555	1728
AAT GCA CCA GAG GGA AAA CAA GAA AAA GCA TCG GTG GTA TTC GGT GCG Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala 560 565 570	1776
AAA CGC CAA CAG CTT GTG CAA TAAGCACGGC T Lys Arg Gln Gln Leu Val Gln 575	1808

b.
cont.

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 599 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe -20 -15 -10 -5
Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser 1 5 10
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu 15 20 25
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala 30 35 40
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn 45 50 55 60

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
65 70 75

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
80 85 90

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
95 100 105

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
110 115 120

Gly Tyr Val Tyr Leu Asn Lys Asn Ile Asp Ile Lys Asn Asn Ile
125 130 135 140

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
145 150 155

Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
160 165 170

Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
175 180 185

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
190 195 200

Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
205 210 215 220

Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
225 230 235

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
240 245 250

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
255 260 265

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
270 275 280

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
285 290 295 300

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
305 310 315

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
320 325 330

Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
335 340 345

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
 350 355 360
 Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
 365 370 375 380
 Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
 385 390 395
 Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
 400 405 410
 Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
 415 420 425
 Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
 430 435 440
 Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
 445 450 455 460
 Ala Ser Asn Gln Glu Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
 465 470 475
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
 480 485 490
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
 495 500 505
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
 510 515 520
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
 525 530 535 540
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
 545 550 555
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
 560 565 570
 Lys Arg Gln Gln Leu Val Gln
 575

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: N. meningitidis
(B) STRAIN: M978

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2115

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGT	CTG	GGT	GGC	GGC	GGC	ACG	TTC	GAT	TCT	GTC	GAT	ACC	GAA		48	
Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu	
1	5						10					15				
GCC	CCG	CGT	CCC	GCC	CCA	AAA	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	CCG	96
Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro	
	20						25					30				
CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCA	ATG	CGC	CTC	AAG	144
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys	
	35						40					45				
CGG	CGG	AAT	TGG	CAT	CCG	CAG	GCA	AAT	CCT	AAA	GAA	GAT	GAG	ATA	AAA	192
Arg	Arg	Asn	Trp	His	Pro	Gln	Ala	Asn	Pro	Lys	Glu	Asp	Glu	Ile	Lys	
b	50					55				60						
CTT	TCT	GAA	AAT	GAT	TGG	GAG	GCG	ACA	GGA	TTG	CCA	GGC	AAT	CCC	AAA	240
Leu	Ser	Glu	Asn	Asp	Trp	Glu	Ala	Thr	Gly	Leu	Pro	Gly	Asn	Pro	Lys	
	65					70				75				80		
AAC	TTA	CCT	GAG	CGA	CAG	AAA	TCG	GTT	ATT	GAA	AAA	GTA	AAA	ACA	GGC	288
Asn	Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Glu	Lys	Val	Lys	Thr	Gly	
	85							90					95			
AGC	GAC	AGC	AAT	ATT	TAT	TCT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	AAC	CAT	336
Ser	Asp	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	
	100					105						110				
CAA	AAC	GGC	AGT	GCA	AAC	CAA	CCA	AAA	AAT	GAA	GTA	AAA	GAT	TAT	AAA	384
Gln	Asn	Gly	Ser	Ala	Asn	Gln	Pro	Lys	Asn	Glu	Val	Lys	Asp	Tyr	Lys	
	115					120						125				
GAG	TTC	AAA	TAT	GTT	TAT	TCC	GGT	TGG	TTT	TAC	AAA	CAC	GCT	AAA	CTC	432
Glu	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His	Ala	Lys	Leu	
	130					135				140						
GAA	ATC	ATA	AAA	GAA	AAC	AAC	TTA	ATT	AAG	GGT	GCA	AAG	AGC	GGC	GAC	480
Glu	Ile	Ile	Lys	Glu	Asn	Asn	Leu	Ile	Lys	Gly	Ala	Lys	Ser	Gly	Asp	
	145					150				155			160			

GAC	GGT	TAT	ATC	TTT	TAT	CAC	GGT	GAA	AAA	CCT	TCC	CGA	CAA	CTT	CCC	528	
Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Glu	Lys	Pro	Ser	Arg	Gln	Leu	Pro		
165									170						175		
GTT	TCT	GGA	GAA	GTT	ACC	TAC	AAA	GGC	GTA	TGG	CAT	TTT	GTA	ACC	GAT	576	
Val	Ser	Gly	Glu	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	Val	Thr	Asp		
180								185					190				
ACG	AAA	CAG	GGA	CAA	AAA	TTT	AAC	GAT	ATT	CTT	GGA	ACC	TCA	AAA	AAA	624	
Thr	-	Lys	Gln	Gly	Gln	Lys	Phe	Asn	Asp	Ile	Leu	Gly	Thr	Ser	Lys	Lys	
195							200					205					
CAA	GGC	GAC	AGG	TAT	AGC	GGA	TTT	CCG	GGT	GAT	GAC	GGC	GAA	GAA	TAT	672	
Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Pro	Gly	Asp	Asp	Gly	Glu	Glu	Tyr		
210						215					220						
TCC	AAT	AAA	AAT	GAA	GCG	ACT	TTA	CAA	GGC	AGT	CAA	GAG	GGT	TAT	GGT	720	
Ser	Asn	Lys	Asn	Glu	Ala	Thr	Leu	Gln	Gly	Ser	Gln	Glu	Gly	Tyr	Gly		
225						230				235					240		
TTT	ACC	TCA	AAT	TTA	AAA	GTG	GAT	TTC	AAT	AAG	AAA	AAA	TTG	ACG	GGT	768	
Phe	Thr	Ser	Asn	Leu	Lys	Val	Asp	Phe	Asn	Lys	Lys	Lys	Leu	Thr	Gly		
245						250				255							
GAA	TTG	ATA	CGC	AAT	AAT	AGA	GTT	ACA	AAC	GCT	ACT	GCT	AAC	GAT	AAA	816	
Glu	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Ala	Asn	Asp	Lys		
260						265				270							
TAC	ACC	ACC	CAA	TAT	TAC	AGC	CTT	GAG	GCT	CAA	GTA	ACA	GGC	AAC	CGC	864	
Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Glu	Ala	Gln	Val	Thr	Gly	Asn	Arg		
275						280				285							
TTC	AAC	GGC	AAG	GCA	ACG	GCA	ACC	GAC	AAA	CCT	GGC	ACT	GGA	GAA	ACC	912	
Phe	Asn	Gly	Lys	Ala	Thr	Ala	Thr	Asp	Lys	Pro	Gly	Thr	Gly	Glu	Thr		
290						295				300							
AAA	CAA	CAT	CCC	TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	GGC	GGC	TTT	960	
Lys	Gln	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	Gly	Gly	Phe		
305						310				315					320		
TTC	GGC	CCG	AAG	GGT	GAG	GAA	TTG	GGT	TTC	CGC	TTT	TTG	AGC	AAC	GAT	1008	
Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	Ser	Asn	Asp		
325						330				335							
CAA	AAA	GTT	GCC	GTT	GTC	GGC	AGC	GCG	AAA	ACC	CAA	GAC	AAA	GCC	GCA	1056	
Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Gln	Asp	Lys	Ala	Ala		
340						345				350							
AAT	GGC	AAT	ACT	GCG	GCG	GCT	TCA	GGC	GGC	ACA	GAT	GCG	GCA	GCA	TCA	1104	
Asn	Gly	Asn	Thr	Ala	Ala	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	Ser		
355						360				365							

AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG GTT	1152
Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val	
370 375 380	
TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT CTC	1200
Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu	
385 390 395 400	
GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG ATT	1248
Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile	
405 410 415	
CCG CTC CTG CCC GAG ACT TCC GAA AGT GGG AGC AAT CAG GCA GAT AAA	1296
Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys	
420 425 430	
GGT AAA AAA GGT AAA AAC GGT AAA AAC GGC GGA ACA GAC TTT ACC TAC	1344
Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr	
435 440 445	
AAA ACA ACC TAC ACG CCG AAA AAC GAT GAC AAA GAT ACC AAA GCC CAA	1392
Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln	
450 455 460	
ACA GGT GCG GCA GGC TCT AGC GGC GCA CAA ACC GAT TTG GGT AAG GCG	1440
Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala	
465 470 475 480	
GAC GTT AAC GGC GGT AAG GCA GAA ACA AAA ACC TAT GAA GTC GAA GTC	1488
Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val	
485 490 495	
TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC GGA ATG TTG ACG CGT AAA	1536
Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys	
500 505 510	
AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA AAC AGT AGT CAA GCT GAT	1584
Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp	
515 520 525	
GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG TTC CTC CAA GGC GAG CGT	1632
Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg	
530 535 540	
ACC GAT GAA AAA GAG ATT CCA AAC GAC CAA AAC GTC GTT TAT CGG GGG	1680
Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly	
545 550 555 560	
TCT TGG TAC GGG CAT ATT GCC AGC AGC ACA AGC TGG AGC GGC AAT GCT	1728
Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala	
565 570 575	

TCC AAT GCA ACG AGT GGC AAC AGG GCG GAA TTT ACT GTG AAT TTC GAT Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp 580 585 590	1776
ACG AAA AAA ATT AAC GGC ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala 595 600 605	1824
ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC AAC GGT TTT TCC GGT ACG Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr 610 615 620	1872
GCA AAA ACT GCT GAC TTA GGT TTT GAT CTC GAT CAA AGC AAT ACC ACC Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr 625 630 635 640	1920
GGC ACG CCT AAG GCA TAT ATC ACA GAT GCC AAG GTG CAG GGC GGT TTT Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe 645 650 655	1968
TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA TGG TTT GCC TAT CCG GGC Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly 660 665 670	2016
GAT AAA CAA ACG GAA AAG GCA ACG GTT GCA TCC GGC GAT GGA AAT TCA Asp Lys Glu Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser 675 680 685	2064
GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val 690 695 700	2112
CAA TAACTAAATG AAGTTGTCTG GGTGGCGGCG GCACGTTCGA TCTTGATTCT Gln 705	2165
GTGCGATACCG AAGCCCCGCG TCCCGCCCCA AAATATCAAG ATGTTCTTC CGAAAAACCG CAAGCCCCAA AAGACCAAGG CGGATACCGT	2225 2255

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
1 5 10 15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
35 40 45

Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys
50 55 60

Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys
65 70 75 80

Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly
85 90 95

Ser Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His
100 105 110

Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys
115 120 125

Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu
130 135 140

Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp
145 150 155 160

Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro
165 170 175

~~8~~
Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp
180 185 190

Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys
195 200 205

Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr
210 215 220

Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly
225 230 235 240

Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly
245 250 255

Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys
260 265 270

Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg
275 280 285

Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr
290 295 300

Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
305 310 315 320

Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp
325 330 335

Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala
340 345 350

Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser
355 360 365

Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val
370 375 380

Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu
385 390 395 400

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
405 410 415

Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys
420 425 430

Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr
435 440 445

Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
450 455 460

Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala
465 470 475 480

Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val
485 490 495

Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys
500 505 510

Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp
515 520 525

Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
530 535 540

Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly
545 550 555 560

Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala
565 570 575

Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp
580 585 590

Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
595 600 605

Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr
610 615 620

Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
625 630 635 640

Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
645 650 655

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
660 665 670

Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser
675 680 685

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val
690 695 700

Gln
705

(2) INFORMATION FOR SEQ ID NO:7:

*b1
ext.*
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. meningitidis
(B) STRAIN: 6940

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2079

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGT TTG GGT GGC GGC GGC ACG TTC GAT CTT GAT TCT GTC GAT ACC GAA
Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
1 5 10 15

GCC CCG CGT CCC GAC CCA AAG TAT CAA GAT GTT TCT TCC GAA AAA CCG	96
Ala Pro Arg Pro Asp Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro	
20 25 30	
CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG ATG AGG TTG AAA	144
Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys	
35 40 45	
CGG AGG AAT TGG TAT TCC GCA GCA AAA GAA GAC GAG GTT AAA CTG AAC	192
Arg Arg Asn Trp Tyr Ser Ala Ala Lys Glu Asp Glu Val Lys Leu Asn	
50 55 60	
GAG AGT GAT TGG GAG ACG ACA GGA TTG CCG ACA GAA CCC AAG AAA CTG	240
Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu	
65 70 75 80	
CCA TTA AAA CAA GAA TCC GTC ATT TCA AAA GTA CAA GCA AAC AAT GGC	288
Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly	
85 90 95	
GAC AAC AAT ATT TAC ACT TCC CCC TAT CTC ACG CAA TCA AAC CAT CAA	336
Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln	
100 105 110	
AAT AGC AGC ATT AAT GGC GGT GCA AAC CTG CCA AAA AAC GAA GTA ACA	384
Asn Ser Ser Ile Asn Gly Gly Ala Asn Leu Pro Lys Asn Glu Val Thr	
115 120 125	
AAT TAT AAA GAT TTC AAA TAT GTT TAT TCC GGC TGG TTT TAT AAA CAT	432
Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His	
130 135 140	
GCT AAA AAC GAA ATC ATA AGA GAA AAC AGC TCA ATT AAG GGT GCA AAG	480
Ala Lys Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys	
145 150 155 160	
AAC GGC GAC GAC GGC TAT ATC TTT TAT CAC GGC AAA GAA CCT TCC CGA	528
Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg	
165 170 175	
CAA CTT CCC GCT TCT GGA ACA GTT ACC TAT AAA GGT GTG TGG CAT TTT	576
Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Val Trp His Phe	
180 185 190	
GCG ACC GAT GTC AAA AAA TCC CAA AAT TTT CGC GAT ATT ATC CAG CCT	624
Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro	
195 200 205	
TCG AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCG GGC GAT GAT GAT	672
Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp	
210 215 220	

GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT CAA GAG Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly Gln Glu 225 230 235 240	720
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AGT AAA AAA Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys 245 250 255	768
TTG ACG GGT AAA TTA ATA CGC AAT AAT AGA GTT ACA AAC GCT CCT ACT Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Pro Thr 260 265 270	816
AAC GAT AAA TAC ACC ACC CAA TAC TAC AGC CTT GAT GCC CAA ATA ACA Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr 275 280 285	864
GGC AAC CGC TTC AAC GGT AAG GCG ATA CGG ACC GAC AAA CCC GAC ACT Gly Asn Arg Phe Asn Gly Lys Ala Ile Arg Thr Asp Lys Pro Asp Thr 290 295 300	912
GGA GGA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser 305 310 315 320	960
GGC GGC TTT TTC GGT CCG AAG GGT GAG GAA TTG GGT TTC CGC TTT TTG Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu 325 330 335	1008
AGC GAC GAT AAA AAA GTT GCG GTT GTC GGC AGC GCG AAA ACC AAA GAC Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp 340 345 350	1056
AAA ACG GAA AAT GGC GCG GTG GCT TCA GGC GGC ACA GAT GCG GCA GCA Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala 355 360 365	1104
TCA AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr 370 375 380	1152
GTT TTG GAT GCG GTC GAG CTG AAA TTG GGC GAT AAG GAA GTC CAA AAG Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys 385 390 395 400	1200
CTC GAC AAC TTC AGC AAC GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met 405 410 415	1248
ATT CCG CTC TTG CCC GAG GCT TCC GAA AGT GGG AAC AAT CAA GCC AAT Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn 420 425 430	1296

CAA GGT ACA AAT GGC GGA ACA GCC TTT ACC CGC AAA TTT GAC CAC ACG Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr 435 440 445	1344
CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly 450 455 460	1392
GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys 465 470 475 480	1440
ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr 485 490 495	1488
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GAA Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu 500 505 510	1536
AGC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met 515 520 525	1584
TTC CTC CAA GGC GAG CGC ACC GAT GAA AAA GAG ATT CCA AGC GAG CAA Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln 530 535 540	1632
AAC ATC GTT TAT CGG GGG TCT TGG TAC GGA TAT ATT GCC AAC GAC AAA Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys 545 550 555 560	1680
AGC ACA AGC TGG AGC GGC AAT GCT TCC AAT GCA ACG AGT GGC AAC AGG Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg 565 570 575	1728
CGC GAA TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACT GGT ACG TTA Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu 580 585 590	1776
ACC GCT GAC AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT AAT ATT Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile 595 600 605	1824
AAG GAC AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe 610 615 620	1872
GAT CTC GAT CAA AGC AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr 625 630 635 640	1920

GAT GCC AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG
Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
645 650 655

1968

GGC GGA TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG AAA AAT GCA ACA
Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr
660 665 670

2016

AAT GCA TCC GGC AAT AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC
Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
675 680 685

2064

CAA CAG CCT GTG CGA TAACGCAAGC CCAAAAAGAC CAAGGCGGAT ACGGT
Gln Gln Pro Val Arg
690

2114

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
1 5 10 15

Ala Pro Arg Pro Asp Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
35 40 45

Arg Arg Asn Trp Tyr Ser Ala Ala Lys Glu Asp Glu Val Lys Leu Asn
50 55 60

Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu
65 70 75 80

Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly
85 90 95

Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln
100 105 110

Asn Ser Ser Ile Asn Gly Gly Ala Asn Leu Pro Lys Asn Glu Val Thr
115 120 125

Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His
130 135 140

Ala Lys Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys
145 150 155 160

Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg
165 170 175

Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Val Trp His Phe
180 185 190

Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro
195 200 205

Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp
210 215 220

Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly Gln Glu
225 230 235 240

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys
245 250 255

Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Pro Thr
260 265 270

Asn Asp Lys Tyr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr
275 280 285

Gly Asn Arg Phe Asn Gly Lys Ala Ile Arg Thr Asp Lys Pro Asp Thr
290 295 300

Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
305 310 315 320

Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu
325 330 335

Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp
340 345 350

Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala
355 360 365

Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr
370 375 380

Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys
385 390 395 400

Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
405 410 415

Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn
420 425 430

Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr
435 440 445

Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
450 455 460

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
465 470 475 480

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
485 490 495

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu
500 505 510

Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
515 520 525

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
530 535 540

Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys
545 550 555 560

Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg
565 570 575

Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu
580 585 590

Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile
595 600 605

Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe
610 615 620

Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr
625 630 635 640

Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
645 650 655

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr
660 665 670

Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
675 680 685

Gln Gln Pro Val Arg
690

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: S3032

(ix) FEATURE:

- (A) NAME/KEY: *mat_peptide*
- (B) LOCATION: 1..2097

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGT TTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT GTC GAT ACC	48
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr	
1 5 10 15	
GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT TCC GAA AAA	96
(Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys	
20 25 30	
CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG ATG AGG TTG	144
Pro Gln Ala Gln Lys Asp Gln Gly Tyr Gly Phe Ala Met Arg Leu	
35 40 45	
AAA CGG AGG AAT TGG TAT CCG TCG GCA AAA GAA AAC GAG GTT AAA CTG	192
Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu	
50 55 60	
AAT GAG AGT GAT TGG GAG ACG ACA GGA TTG CCA AGC AAT CCC AAA AAC	240
Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn	
65 70 75 80	
TTA CCT GAG CGA CAG AAA TCG GTT ATT GAT CAA GTA GAA ACA GAT GGC	288
Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly	
85 90 95	
GAC AGC AAT AAC AGC AAT ATT TAT TCT TCC CCC TAT CTC ACG CAA TCA	336
Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser	
100 105 110	

AAC CAT CAA AAC GGC AAC ACT GGC AAC GGT GTA AAC CAA CCA AAA AAC	384
Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn	
115 120 125	
GAA GTA ACA GAT TAC AAA AAT TTT AAA TAT GTT TAT TCC GGC TGG TTT	432
Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe	
130 135 140	
TAC AAA CAC GCC AAA CGA GAG GTT AAC TTA GCG GTG GAA CCT AAA ATT	480
Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile	
145 150 155 160	
GCA AAA AAC GGC GAC GAC GGT TAT ATC TTC TAT CAC GGT AAA GAC CCT	528
Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro	
165 170 175	
TCC CGA CAA CTT CCC GCT TCT GGA AAA ATT ACC TAT AAA GGT GTG TGG	576
Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp	
180 185 190	
CAT TTT GCG ACC GAT ACA AAA AGG GGT CAA AAA TTT CGT GAA ATT ATC	624
His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile	
195 200 205	
CAA CCT TCA AAA AAT CAA GGC GAC AGA TAT AGC GGA TTT TCG GGT GAT	672
Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp	
210 215 220	
GAT GAT GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT	720
Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly	
225 230 235 240	
CAT GAA GGT TAT GGT TTT GCC TCG AAT TTA GAA GTG GAT TTC GAC AAT	768
His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn	
245 250 255	
AAA AAA TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AAC CAA AAT AAT	816
Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn	
260 265 270	
AAT ACT AAT AAT GAC AAA CAC ACC ACC CAA TAC TAC AGC CTT GAT GCG	864
Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala	
275 280 285	
ACG CTT AAG GGA AAC CGC TTC AGC GGA AAA GCG GAA GCA ACC GAC AAA	912
Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys	
290 295 300	
CCC AAA AAC GAC GGC GAA ACC AAG GAA CAT CCC TTT GTT TCC GAC TCG	960
Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser	
305 310 315 320	

TCT TCT TTG AGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly 325 330 335	1008
TTC CGC TTT TTG AGC AAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala 340 345 350	1056
AAA ACC AAA GAC AAA CCC GCA AAT GGC AAT ACT GCG GAG GCT TCA GGC Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly 355 360 365	1104
GGC ACA GAT GCG GCA GCA TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA Gly Thr Asp Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu 370 375 380	1152
AAC AGT AAG CTG ACC ACG GTT TTG GAT GCG GTC GAG CTG ACG CAC GGC Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly 385 390 395 400	1200
GGC ACA GCA ATC AAA AAT CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu 405 410 415	1248
GTT GTC GAC GGC ATT ATG ATT CCG CTC CTG CCT CAA AAT TCA ACA GGC Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly 420 425 430	1296
AAA AAT AAT CAG CCC GAT CAA GGT AAA AAC GGC GGA ACA GCC TTT ATC Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Thr Ala Phe Ile 435 440 445	1344
TAT AAA ACG ACC TAC ACG CCG AAA AAC GAT GAC AAA GAT ACC AAA GCC Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala 450 455 460	1392
CAA ACA GTC ACG GGC GGC ACG CAA ACC GCT TCA AAT ACG GCA GGT GAT Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp 465 470 475 480	1440
GCC AAT GGC AAA ACA AAA ACG TAT GAA GTC GAA GTC TGC TGT TCC AAC Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn 485 490 495	1488
CTC AAT TAT CTG AAA TAC GGG TTG CTG ACG CGC AAA ACT GCC GGC AAC Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn 500 505 510	1536
ACG GTG GGA AGC GGC AAC AGC AGC CCA ACC GCC GCC GGC CAA ACG GAC Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Gln Thr Asp 515 520 525	1584

Glu Val Lys Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe
125 130 135 140
Tyr Lys His Ala Glu Ser Glu Arg Glu Phe Ser Lys Ile Lys Phe Lys
145 150 155
Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro Ser Arg
160 165 170
Gln Leu Pro Thr Ser Glu Lys Val Ile Tyr Lys Gly Val Trp His Phe
175 180 185
Val Thr Asp Thr Glu Lys Gly Gln Lys Phe Asn Asp Ile Leu Glu Thr
190 195 200
Ser Lys Gly Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly
205 210 215 220
Glu Thr Thr Ser Asn Arg Thr Asp Ser Asn Leu Asn Asp Lys His Glu
225 230 235
Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys
240 245 250
Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Thr
255 260 265
Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr
270 275 280
Gly Asn Arg Phe Asn Gly Lys Ala Ile Ala Thr Asp Lys Pro Asp Thr
285 290 295 300
Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
305 310 315
Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu
320 325 330
Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp
335 340 345
Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala
350 355 360
Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr
365 370 375 380
Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys
385 390 395
Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
400 405 410

Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn Gln Ala Asn
415 420 425

Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr
430 435 440

Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
445 450 455 460

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
465 470 475

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
480 485 490

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu
495 500 505

Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly Gln Ser Met
510 515 520

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
525 530 535 540

Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Ser Ser Thr
545 550 555

β
Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
560 565 570

Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu Thr Ala
575 580 585

Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly
590 595 600

Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu Gly Phe Asp Leu
605 610 615 620

Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
625 630 635

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
640 645 650

Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala
655 660 665

Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
670 675 680

Lys Arg Gln Lys Pro Val Gln
685 690

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1 5 10 15

Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly Lys Glu
35 40 45

Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asn Ser Glu Ser Glu Ser Asn
65 70 75 80

Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly Thr Ala
100 105 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160

Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala Lys Thr Glu Gln Val Glu
165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190

Lys Glu Gln Gln Asp Ile Val
195

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
1 5 10 15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
35 40 45

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60

Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn
65 70 75 80

b
cont. Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
100 105 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160

Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190

Ser Glu Gln Asn Ile Val
195

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1 5 10 15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
20 25 30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
35 40 45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
50 55 60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65 70 75 80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
85 90 95

Lys Phe Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr His Ala Gly
100 105 110

Thr Ala Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr
115 120 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
130 135 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145 150 155 160

Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln
165 170 175

Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
180 185 190

Ile Pro Ser Glu Gln Asn Val
195

GCG CAG AGT ATG TTC CTC CAA GGC GAG CGC ACC GAT GAA AAC AAG ATT Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile 530 535 540	1632
CCA AGC GAG CAA AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile 545 550 555 560	1680
GCC AGC AGC ACA AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly 565 570 575	1728
AAC AGG GCG GAA TTT ACT GTG AAT TTT GGC GAG AAA AAA ATT ACC GGC Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly 580 585 590	1776
ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly 595 600 605	1824
AAG ATT GAG GGC AAC GGT TTT TCC GGT ACG GCA AAA ACT GCT GAA TTA Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu 610 615 620	1872
GGT TTT GAT CTC GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr 625 630 635 640	1920
ATC ACA GAT GCC AAG GTA AAG GGC GGT TTT TAC GGG CCC AAA GCC GAA Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu 645 650 655	1968
GAG TTG GGC GGA TGG TTT GCC TAT TOG GAC GAT AAA CAA ACG AAA AAT Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn 660 665 670	2016
GCA ACA GAT GCA TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val 675 680 685	2064
GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG CAA TAAACCAAGG CGGATAC Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln	2114
690 695	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr
1 5 10 15

Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys
20 25 30

Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu
35 40 45

Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu
50 55 60

Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn
65 70 75 80

Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly
85 90 95

Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser
100 105 110

Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn
115 120 125

Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe
130 135 140

Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile
145 150 155 160

Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro
165 170 175

Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp
180 185 190

His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile
195 200 205

Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp
210 215 220

Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly
225 230 235 240

His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn
245 250 255

Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn
260 265 270

Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala
275 280 285

Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys
290 295 300

Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser
305 310 315 320

Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly
325 330 335

Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala
340 345 350

Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly
355 360 365

Gly Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu
370 375 380

Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly
385 390 395 400

Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu
405 410 415

Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly
420 425 430

Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile
435 440 445

Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala
450 455 460

Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp
465 470 475 480

Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn
485 490 495

Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn
500 505 510

Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp
515 520 525

Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile
530 535 540

Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
545 550 555 560

Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
565 570 575

Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly
580 585 590

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
595 600 605

Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu
610 615 620

Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
625 630 635 640

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
645 650 655

Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
660 665 670

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
675 680 685

Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
690 695

(2) INFORMATION FOR SEQ ID NO:11:

b' wkt.

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: IM2169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1 5 10 15

Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
 65 70 75 80

Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
 85 90 95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160

Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190

Thr Asp Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45

b' 4.
cont.

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
 65 70 75 80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160

Ala Gly Glu Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190

Ser Glu Gln Asn Ile Val
 195

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: 2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45

*β
cont.*

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65 70 75 80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
100 105 110

Ala Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160

Ala Gly Glu Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190

Ser Glu Gln Asn Ile Val
195

b
cont.
(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: C708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Gly
1 5 10 15

Ala Ala Arg Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn
65 70 75 80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95

Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
100 105 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160

Ala Gly Glu Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190

Asn Asp Gln Asn Val Val
195

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: M978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ser Gly Gly
1 5 10 15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
20 25 30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
35 40 45

*b1
cont.*

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
50 55 60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
65 70 75 80

Ser Asn Gln Ala Asp Lys Gly Lys Gly Lys Asn Gly Lys Asn Gly
85 90 95

Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp
100 105 110

Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln
115 120 125

Thr Asp Leu Gly Lys Ala Asp Val Asn Gly Gly Lys Ala Glu Thr Lys
130 135 140

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
145 150 155 160

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
165 170 175

Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
180 185 190

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
195 200 205

Asn Val Val
210

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Arg Asp Lys Ala Glu Ser Gly Gly Asn Gly Ala Ser Gly Gly
1 5 10 15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
20 25 30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly
35 40 45

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
50 55 60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65 70 75 80

Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Lys Phe Thr Arg
85 90 95

Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
100 105 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
115 120 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
130 135 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145 150 155 160

Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln
165 170 175

Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
180 185 190

Ile Pro Ser Glu Gln Asn Val Val
195 200

*b
cont.*

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: 867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Lys Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
1 5 10 15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys
 20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
 35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Ala
 50 55 60

Gly Ile Met Ile Pro Leu Met Pro Glu Thr Ser Glu Ser Gly Asn Asn
 65 70 75 80

Gln Ala Asp Leu Gly Leu Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95

Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Pro
 100 105 110

Thr Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Val Thr Gly Gly
 115 120 125

Gln Ala Gly Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn
 130 135 140

Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Val
 145 150 155 160

Gly Ser Gly Asn Gly Ser Ser Thr Ala Ala Ala Gln Thr Ala Gln Gly
 165 170 175

Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile
 180 185 190

Pro Lys Glu Gln Gln Asp Ile Val
 195 200

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: S3032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1 5 10 15

Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn
20 25 30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly
35 40 45

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
50 55 60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys
65 70 75 80

Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr
85 90 95

Leu Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
100 105 110

Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala
115 120 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
130 135 140

Asn Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145 150 155 160

Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala
165 170 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro
180 185 190

Ser Glu Gln Asn Val Val
195

b' CNT.

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr Lys Asp Lys Pro Gly Asn Gly Ala Arg Leu Gln Ala Ala Arg Cys
1 5 10 15

Gly Thr Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys Leu
20 25 30

Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val
35 40 45

Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly
50 55 60

Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Lys Asn Gln
65 70 75 80

Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe Glu
85 90 95

His Thr Pro Glu Ser Asp Glu Lys Asp Ala Gln Ala Gly Thr Pro Ser
100 105 110

Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys
115 120 125

Thr Lys Thr Tyr Glu Val Asn Leu Cys Ser Asn Leu Asn Tyr Leu Lys
130 135 140

Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly
145 150 155 160

Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met
165 170 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
180 185 190

Asn Val Val
195

B' cont.

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAACCCGGAT CCGTTGCCAG CGCTGCCGT

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTCATG AGATATCTGG CAACATTGTT GTTATCTCTG GCGGTGTTAA TCACCGCCGG 60

GTGCCTGGGT GGCGGCGGCA GTTTC 85

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

b
cut
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGTTTTGT TGAGTGCATG -CCTGGGTGGC 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGCGCAAGCT TACAGTTGT CTTTGGTTTT CGCGCTGCCG 40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAAAGCATG CATAAAAAC TACGCAGTACCA CCATTCAAGC

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATATAAGCT TACGTTGCAG GCCCTGCCGC GTTTTCCCC

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCT GCCGTCTGAA GCCTTATTC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCCGAATTCT GCTATGGTGC TGCCTGTG

28

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGCATCCAAA ACCGTACCTG TGCTGCCCTGA

30

(2) INFORMATION FOR SEQ ID NO:29:

B
last.
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTATCACTT TCCGGGGGCA GGAGCGGAAT

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTTGGAACAG CAGACAGCGG TTTGCGCCCC

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAACATACTT TGTCGTTTT TGCGCGTCAA

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

b
cont. (vi) ORIGINAL SOURCE:
(A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Lys Gly Thr Trp
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

B'
cont.

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Val Phe Gly Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2067

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..60

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 61..2067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Ieu Pro Val Phe -20 -15 -10 -5	48
TTG TTG AGT GCT TGT CTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser 1 5 10	96
GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser 15 20 25	144
TCC GAA ACA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala 30 35 40	192
ATG CGC TTC AAG CGG CGG AAT TGG TAC CCA AAA AAT GAA GAA GAT CAT Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His 45 50 55 60	240
AAG GCA TTA TCA GAA GCG GAT TGG GAG AAG TTA GGT GCG GGT AAG CCA Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro 65 70 75	288
GAT GAG TTT CCC CAA AGG AAT GAA ATA TTG AAT ATG ACT GAC GGA ATT Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile 80 85 90	336
CTG AGT GAG TCT CTT CAG CTG GGT GAG GGC GGC AAA AGC CGC GTA GAA Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu 95 100 105	384
GGA TAC ACG GAT TTC CAA TAT GTC CGC TCG GGC TAT ATC TAC CGC AAC Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn 110 115 120	432

GGT	GCC	AAT	AAA	ATC	GAT	TTC	CAA	AAA	AAA	ATC	GCC	CTT	TCC	GGT	CCG		480
Gly	Ala	Asn	Lys	Ile	Asp	Phe	Gln	Lys	Lys	Ile	Ala	Leu	Ser	Gly	Pro		
125				130					135						140		
GAC	GGC	TAC	CTT	TTC	TAC	AAA	GGC	AGC	AAT	CCT	TCC	CAA	GCT	CTG	CCG		528
Asp	Gly	Tyr	Leu	Phe	Tyr	Lys	Gly	Ser	Asn	Pro	Ser	Gln	Ala	Leu	Pro		
145									150						155		
ATG	GGT	AAG	GTA	GGT	TAT	AAA	GGT	ACT	TGG	GAT	TAT	GTA	ACC	GAT	GCC		576
Met	Gly	Lys	Val	Gly	Tyr	Lys	Gly	Thr	Trp	Asp	Tyr	Val	Thr	Asp	Ala		
								160	165				170				
AAG	ATG	GGA	CAA	AAA	TTT	TCC	CAG	TTG	GCT	GGT	TTT	CCA	GCG	GGG	GAT		624
Lys	Met	Gly	Gln	Lys	Phe	Ser	Gln	Leu	Ala	Gly	Phe	Pro	Ala	Gly	Asp		
175							180					185					
AGG	TAT	GGG	GCT	TTG	TCT	GCC	GAG	GAA	GCG	GAT	GTG	TTG	CGC	AAC	AAA		672
Arg	Tyr	Gly	Ala	Leu	Ser	Ala	Glu	Glu	Ala	Asp	Val	Leu	Arg	Asn	Lys		
190							195					200					
AGC	GAG	GCA	CAG	CAA	GGT	CAG	ACC	GAT	TTC	GGG	CTG	ACC	AGC	GAG	TTT		720
Ser	Glu	Ala	Gln	Gly	Gln	Gly	Gln	Thr	Asp	Phe	Gly	Leu	Thr	Ser	Glu	Phe	
205							210				215				220		
GAG	GTG	GAT	TTC	GCC	GCC	AAG	ACC	ATG	ACC	GGC	GCG	CTC	TAC	CGC	AAT		768
Glu	Val	Asp	Phe	Ala	Ala	Lys	Thr	Met	Thr	Gly	Ala	Leu	Tyr	Arg	Asn		
225									230						235		
AAC	CGG	ATT	ACT	AAT	AAC	GAA	ACC	GAA	AAT	AAA	GCC	AAA	CAA	ATT	AAA		816
Asn	Arg	Ile	Thr	Asn	Asn	Glu	Thr	Glu	Asn	Lys	Ala	Lys	Gln	Ile	Lys		
240							245						250				
CGT	TAC	GAC	ATT	CAG	GCT	GAC	CTG	CAC	GGT	AAC	CGC	TTC	AGC	GGC	AAG		864
Arg	Tyr	Asp	Ile	Gln	Ala	Asp	Leu	His	Gly	Asn	Arg	Phe	Ser	Gly	Lys		
255							260					265					
GCA	ACG	GCA	ACC	GAC	AAA	C/C	AAA	AAC	GAC	GAA	ACC	AAG	GAA	CAT	CCC		912
Ala	Thr	Ala	Thr	Asp	Lys	Pro	Lys	Asn	Asp	Glu	Thr	Lys	Glu	His	Pro		
270							275					280					
TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	GGC	GGC	TTT	TTC	GGT	CCG	AAG		960
Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Lys		
285							290				295				300		
GGT	GAG	GAA	TTG	GGT	TTC	CGC	TTT	TTG	AGC	GAC	GAT	CAA	AAA	GTT	GCC		1008
Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	Ser	Asp	Asp	Gln	Lys	Val	Ala		
305									310						315		
GTT	GTC	GGC	AGC	GCG	AAA	ACC	AAA	GAC	AAA	CTG	GAA	AAT	GGC	GCG	GCG		1056
Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	Lys	Leu	Glu	Asn	Gly	Ala	Ala		
320								325					330				

GCT TCA GGC AGC ACA GGT GCG GCA GCA TCG GGC GGT GCG GCA GAT ATG Ala Ser Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met 335 340 345	1104
CCG TCT GAA AAC GGT AAG CTG ACC ACG GTT TTG GAT GCG GTT GAG CTG Pro Ser Glu Asn Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu 350 355 360	1152
AAA TCT GGC GGT AAG GAA GTC AAA AAT CTC GAC AAC TTC AGC AAT GCC Lys Ser Gly Gly Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala 365 370 375 380	1200
GCC CAA CTG GTT GTC GAC GGC ATT ATG ATT CCG CTC CTG CCC AAG AAT Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asn 385 390 395	1248
TCC GAA AGC GAG AGC AAT CAG GCA GAT AAA GGT AAA AAC GGC GGA ACA Ser Glu Ser Glu Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr 400 405 410	1296
GCC TTT ACC CGC AAA TTT GAA CAC ACG CCG GAA AGT GAT AAA AAA GAC Ala Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp 415 420 425	1344
ACC CAA GCA GGT ACG GCG GAG AAT GGC AAT CCA GCC GCT TCA AAT ACG (Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr 430 435 440	1392
<i>b</i> GCA GGT GAT ACC AAT GGC AAA ACA AAA ACC TAT GAA GTC GAA GTC TGC Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys 445 450 455 460	1440
TGT TCC AAC CTC AAT TAT CTG AAA TAC GGA ATG TTG ACG CGT AAA AAC Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn 465 470 475	1488
AGC AAG TCC GCG ATG CAG GCA GGC GAA AAC GGT AGT CTA GCT GAC GCT Ser Lys Ser Ala Met Gln Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala 480 485 490	1536
AAA ACG GAA CAA GTT GAA CAA AGT ATG TTC CTC CAA GGC GAG CGC ACC Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr 495 500 505	1584
GAT GAA AAA GAG ATT CCA AAA GAG CAA CAA GAC ATC GTT TAT CGG GGG Asp Glu Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly 510 515 520	1632
TCT TGG TAC GGG CAT ATT GCC AAC GAC ACA AGC TGG AGC GGC AAT GCT Ser Trp Tyr Gly His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala 525 530 535 540	1680

TCA GAT AGA GAG GGC GGC AAC AGG GCG GAC TTT ACC GTG AAT TTT GGT Ser Asp Arg Glu Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly 545 550 555	1728
ACG AAA AAA ATT AAC GGA ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala 560 565 570	1776
ACC TTT ACC ATT GTG GGC GAT ATT AAG GAC AAC GGC TTT GAA GGT ACG Thr Phe Thr Ile Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr 575 580 585	1824
GCG AAA ACT GCT GAC TCA GGT TTT GAT CTC GAT CAA AGC AAT ACC ACC Ala Lys Thr Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr 590 595 600	1872
CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC AAG GTG AAG GGC GGT TTT Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe 605 610 615 620	1920
TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA TGG TTT GCC TAT CCG GGC Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly 625 630 635	1968
<i>GAT AAA CAA ACG GAA AAG GCA ACG GTT ACA TCC GGC GAT GGA AAT TCA</i> <i>Asp Lys Gln Thr Glu Lys Ala Thr Val Thr Ser Gly Asp Gly Asn Ser</i> <i>640 645 650</i>	2016
<i>cont.</i>	
GCA AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC CAA AAG CCT GTG Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Lys Pro Val 655 660 665	2064
CAA TAAAGTTTCG ATCTTGATTC TGTGATACC GAAGCCCCGC GTCCCGCGCC AAATAAAA Gln	2125

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe -20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser 1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His
45 50 55 60

Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro
65 70 75

Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile
80 85 90

Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Lys Ser Arg Val Glu
95 100 105

Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn
110 115 120

Gly Ala Asn Lys Ile Asp Phe Gln Lys Lys Ile Ala Leu Ser Gly Pro
125 130 135 140

Asp Gly Tyr Leu Phe Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro
145 150 155

Met Gly Lys Val Gly Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala
160 165 170

Lys Met Gly Gln Lys Phe Ser Gln Leu Ala Gly Phe Pro Ala Gly Asp
175 180 185

Arg Tyr Gly Ala Leu Ser Ala Glu Glu Ala Asp Val Leu Arg Asn Lys
190 195 200

Ser Glu Ala Gln Gln Gly Gln Thr Asp Phe Gly Leu Thr Ser Glu Phe
205 210 215 220

Glu Val Asp Phe Ala Ala Lys Thr Met Thr Gly Ala Leu Tyr Arg Asn
225 230 235

Asn Arg Ile Thr Asn Asn Glu Thr Glu Asn Lys Ala Lys Gln Ile Lys
240 245 250

Arg Tyr Asp Ile Gln Ala Asp Leu His Gly Asn Arg Phe Ser Gly Lys
255 260 265

Ala Thr Ala Thr Asp Lys Pro Lys Asn Asp Glu Thr Lys Glu His Pro
270 275 280

Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys
285 290 295 300

Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala
305 310 315

Val Val Gly Ser Ala Lys Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala
320 325 330

Ala Ser Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met
335 340 345

Pro Ser Glu Asn Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu
350 355 360

Lys Ser Gly Gly Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala
365 370 375 380

Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asn
385 390 395

Ser Glu Ser Glu Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr
400 405 410

Ala Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp
415 420 425

Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr
430 435 440

Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys
445 450 455 460

Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn
465 470 475

Ser Lys Ser Ala Met Gln Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala
480 485 490

Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
495 500 505

Asp Glu Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly
510 515 520

Ser Trp Tyr Gly His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala
525 530 535 540

Ser Asp Arg Glu Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly
545 550 555

Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
560 565 570

Thr Phe Thr Ile Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr
575 580 585

Ala Lys Thr Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
590 595 600

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe
605 610 615 620

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
625 630 635

Asp Lys Gln Thr Glu Lys Ala Thr Val Thr Ser Gly Asp Gly Asn Ser
640 645 650

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Lys Pro Val
655 660 665

Gln

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

b
cont.
(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2133

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..2133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

48

TTG TTG AGT GCT TGT TTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT
Leu Leu Ser Ala Cys Leu Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

96

GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAA TAT CAA GAT GTT TCT	144
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG	192
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
ATG AGG TTG AAA CGG AGG AAT CGG CAT CCG CAG GCA AAA GAA GAC AAA	240
Met Arg Leu Lys Arg Arg Asn Arg His Pro Gln Ala Lys Glu Asp Lys	
45 50 55 60	
GTT GAA CTA AAC CCA AAT GAT TGG GAG GAG ACA GGA TTG CCG AGC AAG	288
Val Glu Leu Asn Pro Asn Asp Trp Glu Glu Thr Gly Leu Pro Ser Lys	
65 70 75	
CCC CAA AAC TTA CCC GAG CGA CAG CAA TCG GTT ATT GAT AAA GTA AAA	336
Pro Gln Asn Leu Pro Glu Arg Gln Gln Ser Val Ile Asp Lys Val Lys	
80 85 90	
ACA GAC GAT GGC AGC AAT ATT TAC ACT TCC CCT TAT CTC ACG CAA TCA	384
Thr Asp Asp Gly Ser Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser	
95 100 105	
AAC CAT CAA AAC GGC AGC ACT AAT AGC GGT GCA AAC CAA CCA AAA AAC	432
Asn His Gln Asn Gly Ser Thr Asn Ser Gly Ala Asn Gln Pro Lys Asn	
110 115 120	
GAA GTA AAA GAT TAC AAA AAT TTC AAA TAT GTT TAT TCC GGC TGG TTT	480
Glu Val Lys Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe	
125 130 135 140	
TAT AAA CAT GCA GAG AGT GAA AGA GAA TTC AGT AAA ATC AAA TTT AAG	528
Tyr Lys His Ala Glu Ser Glu Arg Glu Phe Ser Lys Ile Lys Phe Lys	
145 150 155	
TCA GGC GAC GAC GGC TAT ATT TTT TAT CAC GGT AAA GAC CCT TCC CGA	576
Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro Ser Arg	
160 165 170	
CAA CTT CCC ACT TCT GAA AAA GTT ATC TAC AAA GGC GTA TGG CAT TTT	624
Gln Leu Pro Thr Ser Glu Lys Val Ile Tyr Lys Gly Val Trp His Phe	
175 180 185	
GTA ACC GAT ACT GAA AAG GGA CAA AAA TTT AAC GAT ATT CTT GAA ACC	672
Val Thr Asp Thr Glu Lys Gly Gln Lys Phe Asn Asp Ile Leu Glu Thr	
190 195 200	
TCA AAA GGG CAA GGC GAC AGA TAC AGC GGA TTT TCG GGC GAT GAC GGC	720
Ser Lys Gly Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly	
205 210 215 220	

GAA ACA ACT TCC AAT AGA ACT GAT TCC AAC CTT AAT GAT AAG CAC GAG Glu Thr Thr Ser Asn Arg Thr Asp Ser Asn Leu Asn Asp Lys His Glu 225 230 235	768
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AGT AAA AAA Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys 240 245 250	816
TTG ACG GGT AAA TTA ATA CGC AAT AAT AGA GTT ACA AAC GCT ACT ACT Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Thr 255 260 265	864
AAC GAT AAA TAC ACC ACC CAA TAC TAC AGC CTT GAT GCC CAA ATA ACA Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr 270 275 280	912
GGC AAC CGC TTC AAC GGT AAG GCG ATA GCG ACC GAC AAA CCC GAC ACT Gly Asn Arg Phe Asn Gly Lys Ala Ile Ala Thr Asp Lys Pro Asp Thr 285 290 295 300	960
GGA GGA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser 305 310 315	1008
GGC GGC TTT TTC GGT CCG AAG GGT GAG GAA TTG GGT TTC CGC TTT TTG (Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu 320 325 330	1056
AGC GAC GAT AAA AAA GTT GCG GTT GTC GGC AGC GCG AAA ACC AAA GAC Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp 335 340 345	1104
AAA ACG GAA AAT GGC GCG GTG GCT TCA GGC GGC ACA GAT GCG GCA GCA Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala 350 355 360	1152
TCA AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr 365 370 375 380	1200
GTT TTG GAT GCG GTC GAG CTG AAA TTG GGC GAT AAG GAA GTC CAA AAG Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys 385 390 395	1248
CTC GAC AAC TTC AGC AAC GCC GGC CAA CTG GTT GTC GAC GGC ATT ATG Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met 400 405 410	1296
ATT CCG CTC TTG CCC GAG ACT TCC GAA AGT GGG AAC AAT CAA GCC AAT Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn Gln Ala Asn 415 420 425	1344

CAA GGT ACA AAT GGC GGA ACA GCC TTT ACC CGC AAA TTT GAC CAC ACG Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr 430 435 440	1392
CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly 445 450 455 460	1440
GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys 465 470 475	1488
ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr 480 485 490	1536
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GAA Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu 495 500 505	1584
AGC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GGA CAA AGT ATG Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly Gln Ser Met 510 515 520	1632
TTC CTC CAA GGC GAG CGC ACC GAT GAA AAA GAG ATT CCA AGC GAG CAA Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln 525 530 535 540	1680
AAC ATC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AGC AGC ACA Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Ser Ser Thr 545 550 555	1728
AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGC AGG GCG GAA Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu 560 565 570	1776
TTT ACT GTG AAT TTT GGC GAG AAA AAA ATT ACC GGC ACG TTA ACC GCT Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu Thr Ala 575 580 585	1824
GAA AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly 590 595 600	1872
AAC GGT TTT TCC GGT ACG GCA AAA ACT GCT GAA TTA GGT TTT GAT CTC Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu Gly Phe Asp Leu 605 610 615 620	1920
GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala 625 630 635	1968

AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG GGC GGA
Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
640 645 650

2016

TGG TTT GCC TAT CAG GGC GAT AAA CAA ACG GAA AAT ACA ACA GTT GCA
Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala
655 660 665

2064

TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC GTA TTC GGT GCG
Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
670 675 680

2112

AAA CGC CAA AAG CCT GTG CAA TAAAGTAAAA
Lys Arg Gln Lys Pro Val Gln
685 690

2143

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

b' cerel. (ii) MOLECULE TYPE: protein

b' cerel. (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

Met Arg Leu Lys Arg Arg Asn Arg His Pro Gln Ala Lys Glu Asp Lys
45 50 55 60

Val Glu Leu Asn Pro Asn Asp Trp Glu Glu Thr Gly Leu Pro Ser Lys
65 70 75

Pro Gln Asn Leu Pro Glu Arg Gln Gln Ser Val Ile Asp Lys Val Lys
80 85 90

Thr Asp Asp Gly Ser Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser
95 100 105

Asn His Gln Asn Gly Ser Thr Asn Ser Gly Ala Asn Gln Pro Lys Asn
110 115 120